

1/24

GTTCACGC

1
10 AGCAGTACCACACCACGATCAACCGCATATTTCAGTTTGGAGCACATTGCCAATTTCAAGATGTTGACAAAGTTGGCTCTATGGCACTACCACCTCTACTGGGAGGATGTGT
125 ACCCTGTATTGATCGTGGAGGATGTCAGCTCCACAACTGCACGCTGGAGTTTCGGTTACGCTATCGCAATTCATTAACACTCCAACTACAGCGACTTGTGTGTCGTATGTC
240 TGAAGGCAACGGCTTGGCGTCTGAACGGTACAGAGAGTTTTCGATATGGAACGGAGAGACTTTTCAAGTTTGGAGAGCTTACGGTCACTGTGGCGAGAGGGAGTCTC
355 AACAGCAGCGTATGTCAUGGTTCAAGACTGGCACTTCCGAGACTAAGAGCATTTGGGGTTCTTGGAGGAGGGCGCATACACCTATGCCATTGGTTTGGAAAGTTGC
470 CGACAAACAGCTAGCTTGGGGTACTAGACATGCGAGGTGGATTACGAAGCTCGTGACCGGGAGAGAGCATTTGAAGGAGGCCAATAGATACTTTCCATTCTCTGATGTGAAGATAC
585 ATAGACCATAAAGCACAAGGCTGGGAATATATACGGGTATAGACTCTACTAATAACATCCAAACAGAGTGAAATAAATAACACACAAACAGAGAAATAACAAACGA
700 ACCACTTACAGAGCCCATCTTACACACACACCATATACGGGTATAGCTCTACTAATAACATCCAAACAGAGTGAAATAAATAACACACAAACAGAGAAATAACAAACGA
815 AATATTGTACCGACCCGTCACCCATATCCAGGATGCGAGGTTCCAGTTTCAACACCCACCCACACAGTACTACTAGACTACCCCATTTGGATCTATCGAGG
930 ACCAGGATATGTCACATTAATCACAGTCACATACGATACCGTTGGCAACCGATCAACACTACTAGTGGCGTGAACACTACGGAGACATACGTTTACGACGGCGACAT
1045 GCTCACAATTAGCTATGCTGGCGCCACCATGCCGTAGCACTTTAGCATTGACATGCTGTATATGCACAGCAACGAGTTGGTTGAGAGTGTGGAGGATGAGTTTGATTTGTAT
1160 GTGGCGGTACCTACGAGTTCCATGCCCTTTAGTTATGACAAATGGCAGGTTTTCGAAGAGAAACCGCATTTGCTTCCAAATTTGACGTAACAAATTTGCCAGTAGATTCTTTAC
1275 CCATTCCATTGGAGTTGTACGAACAATCGTGTATTTAGTAGATATCACATATTCATTGCTGGAACATCTTCCCATATTTGGTTAAGGCTGTATTAGAGCCGTGGGGCAGTA
1390 GTGTTCGTTATATTTAAGCAAAATAAACAATGATTTTATCAAGTCGATAGCCTTATACATTTAGCTGATATGTTTGTCTATAGGTTTAAATGATATTTAGATTTA
1505 AGGTTTGTGTAGCTGGCAAGTTTATAGATGCCAATTCGTTGGGTCGTTCCTACCAATACTGCAGTAAGAGAGTTTGAAGTTTGTATATATTTAGCTCATTTCGCAG
1620 ATCAATAATTGCTTTCTTTCTAGGTGCCACACTACCAAAAGGTTATGGTTAAGAGGACACCGTGCATTTCCTGTTCCCTAAGCCAATGACATACCGCTCTCCCAATATA
1735 AGAGATCGGGGCTTGAAACGTTTTCAGATGAAGTTATGCGAAGTCTTTGCTCTATGATGAGCAAGATTAGTTGCCCAATATATACAGGACAGAGTTCAAGTTGGAA

FIG. 1A

1850 ATTATATGAATGTATCTCTGATTAAGCGGAACTATGGGCGCTAAATGTCAATCACCAGCAAAAGATATACCTAAGGTTAAGAGAAATCATCAATGATAAATGTTTCTCCCCCATG
1965 GGTGATATAGTAGGACACCTTACTTCTCATGAATTAACACACAATTTGTATATAGTCTCAGCATAGTAAGTTCTACAAGTTTTTGGACAAAATAAGTCCAGATACGACGACATACAT
2080 GTAGGGAGCCAAACAAAATATTTATCCGAGCAAAACAGGTTGCTAGAGGTGATTATATATCCGGAGTTAGTATCTGTACAGAGACAAAGGCTCAAGGAATTAAGCAAAACC
2195 AAAGTTTGGCAATGAAGCAAAAGTTTNGAGCTGAATTCAAAAATTAATAACCTATCGGTGGCTCGCAAGGATCTTACACAGCAATTTCTAGAGCGGCAGAGCGTGGTTG
2310 AGAGATTCAAAATGGTGTATAGTGAATTCAGAAATGCCAGAAACCGAANGTGTCCCAAGAGAGCAGTAGCAGACAACTCAGGTGGAGCTTATCGGTCTACAGAGAGTAAACCAAGTTG
2425 GAACATTGCTAATGATNTCAATTTTACATCGGACACTGAGNAACTCCAAATTCACCTGATTAACCGGAACCGCCGATACCTCCAGGAGATAATTTGATTTAACTTCAGATAC
2540 AGAAGACATAGAGCCACATCACCAGAGGTAATGATATAGTAAGTTAAATATAAGGCAAAATATTTGCCAATGTATACTCTTTTAACAGTGTGTTCTCTGTCAGAGGATT
2655 AAGCACCAGAAAAAATATGTGGATCGGTGTTATAGTTTACTCTTTCTGAAAAAGAACATTAACTGTTCTTACTAGTTGTCCACACTAGCAGACACAGTCCCTGAA
29 Met Ser Phe Ala Arg Tyr Ile Tyr Tyr Thr Ile Ala Val Ala Val Leu Leu Asn Phe Val Lys Ala Thr Glu Asn Asn Phe Lys
58 2770 ATG TCA TTT GCA AGG TAT ATC TAC TAC ACC ATT GCG GTT GCT GGT TTA TTA AAT TTT GTC AAA GCT ACT GAA AAT AAC AAT TTT AAA
Leu Glu Val Glu Ala Ser Trp Ser Asn Ile Asp Phe Leu Pro Ser Phe Ile Glu Ala Ile Val Gly Phe Asn Asp Ser Leu Tyr Glu
87 2857 CTT GAA GTT GAA GCG TCA TGG AGC AAT ATT GAT TTC CTT CCT AGC TTT ATA GAG GCC ATC GTT GGC TTC AAT GAC TCT TTG TAC GAA
Gln Thr Ile Glu Thr Ile Phe Gly Leu Gly Asp Thr Glu Val Glu Leu Glu Asp Ala Ser Asp Gln Glu Ile Tyr Ser Thr Val
116 2944 CAG ACA ATT GAA ACA ATT TTT GGT TTA GGA GAC ACT GAA GTG GAA TTA GAA GAT GAT GCT TCA GAT CAA GAA ATA TAT TCT ACC GTG
Ile Asn Ser Leu Gly Leu Thr Asp Gln Asp Leu Asp Phe Ile Asn Phe Asp Leu Thr Asn Lys His Thr Pro Arg Ile Ala Ala
145 3031 ATC AAC TCA TTA GGG' TTA ACA GAT CAA GAT TTG GAT TTT AAT TTT GAT TTA ACC AAC AAA AAA CAT ACA CCA AGA ATC GCA GCC
His Tyr Asp His Tyr Ser Asp Val Leu Thr Lys Phe Gly Asp Arg Leu Lys Ser Glu Cys Ala Lys Asp Ser Phe Gly Asn Ala Val
174 3118 CAT TAC GAT CAC TAT TCT GAT GTT CTA ACT AAG TTT GGC GAT CGA CTC AAA AGT GAA TGT GCA AAA GAC TCT TTT GGG AAT GCA GTG
Glu Thr Lys Asn Gly Gln Ile Gln Thr Trp Leu Leu Tyr Asn Asp Lys Ile Tyr Cys Ser Ala Asn Asp Leu Phe Ala Leu Arg Thr

~~FIGURE 1A~~ - 1A (cont.)

3205 GAA ACG AAA AAT GGT CAA ATT CAA ACG TGG TTA CTA TAT AAC GAT AAG ATA TAT TGT TCG GCT AAT GAT TTG TTT GCA TTA CGA ACT
 Asp Leu Ser Ser His Ser Thr Leu Leu Phe Asp Arg Ile Ile Gly Lys Ser Lys Asp Ala Pro Leu Val Ile Leu Tyr Gly Ser Pro 203
 3292 GAT TTG AGT TCT CAT TCT ACA CTT TTA TTT GAT AGG ATT ATT GGA AAA TCA AAA GAT GCA CCT TTG GTG ATT TTA TAT GGA AGC CCG
 Thr Glu Glu Leu Thr Lys Asp Phe Leu Lys Ile Leu Tyr Pro Asp Ala Lys Ala Gly Lys Leu Lys Phe Val Trp Arg Tyr Ile Pro 232
 3379 ACT GAG GAA CTG ACT AAA GAT TTT CTT AAA ATA TTG TAT CCA GAT GCA AAG GCT GGA AAA TTA ANG TTT GTA TCG AGG TAC ATT CCA
 Leu Gly Ile Lys Lys Leu Asp Ser Ile Ser Gly Tyr Gly Val Ser Leu Lys Met Glu Lys Tyr Asp Tyr Ser Gly Ala Glu Gly Asn 261
 3466 CTG GGA ATC AAA AAA CTG GAC TCA ATT TCT GCA TAC TCA TTA TTA AAA ATG GAA AAG TAT GAT TAT TCT GGT GCA GAA GGA AAT
 Pro Lys Tyr Asp Leu Ser Arg Asp Phe Thr Arg Ile Asn Asp Ser Gln Glu Leu Val Asn Glu Lys His Ser Tyr Glu Leu 290
 3553 CCA AAG TAT GAT TTG AGT CGA GAT TTC ACC ACA ATT AAT GAC TCG CAA GAG TTG GTC CTG GTC AAT GAA AAA CAT TCG TAT GAA CTT
 Gly Val Lys Leu Thr Ser Phe Ile Leu Ser Asn Arg Tyr Lys Ser Thr Lys Tyr Asp Leu Leu Asp Thr Ile Leu Thr Asn Phe Pro 319
 3640 GGT GTT AAA TTG ACT TCA TTC ATA TTA TCC AAT CGT TAC AAG ACT AAA TAT GAC CTT TTA GAT ACG ATT TTA ACC AAC TTT CCC
 Lys Phe Ile Pro Tyr Ile Ala Arg Leu Pro Lys Leu Leu Asn His Glu Lys Val Lys Ser Lys Val Leu Gly Asn Glu Asp Ile Gly 348
 3727 AAG TTT ATT CCT TAC ATT GCA CGA TTA CCA AAA TTA CTA AAT CAT GAA AAA GTT AAA TCC AAA GTG CTT GCA AAT GAA GAT ATA GGG
 Leu Ser Gln Asp Ser Tyr Gly Ile Tyr Ile Asn Gly Ser Pro Ile Asn Pro Leu Glu Leu Asp Ile Tyr Asn Leu Gly Thr Arg Ile 377
 3814 CTA TCT CAA GAC TCC TAC GCA ATA TAT ATC AAC GGT TCC CCA ATA AAT CCA CTA GAG TTA GAT ATT TAC AAT CTA GGT ACC AGG ATA
 Lys Glu Glu Leu Gln Thr Val Lys Asp Leu Val Lys Leu Gly Phe Asp Thr Val Gln Ala Lys Leu Ile Ala Lys Phe Ala Leu 406
 3901 ANG GAG GAA TTA CAG ACT GTG AAA GAT TTA GTG NAA CTT GGA TTT GAT ACC GTA CAA GCA AAG CTC TTG ATA GCA AAA TTT GCT TTA
 Leu Ser Ala Val Lys Gln Thr Phe Arg Asn Gly Asn Thr Leu Met Gly Asn Asn Glu Asn Arg Phe Lys Val Tyr Glu Asn Glu 435
 3988 CTT TCA GCT GTT AAA CAA ACA CAA TTT CGA AAT GGG AAT ACA TTA ATG GGT AAC AAT GAA AAT AGA TTT AAA GTG TAT GAA AAT GAA
~~718105~~ - 1A (cont.)

464 Phe Lys Lys Gly Ser Ser Glu Lys Gly Gly Val Leu Phe Phe Asn Asn Ile Glu Leu Asp Asn Thr Phe Lys Glu Tyr Thr Thr Asp
4075 TTT AAG AAG GGT AGT TCA GAA AAG GGT GGG GTC TTG TTT TTC AAT AAC ATT GAA TTA GAC AAC ACA TTC AAG GAG TAC ACC ACT GAT
493 Arg Glu Glu Ala Tyr Leu Gly Val Gly Ser His Lys Lys Leu Lys Pro Asn Gln Ile Pro Leu Leu Lys Glu Asn Ile His Asp Leu Ile
4162 CGT GAG GAG GCA TAT TTA GCA GTT GGT TCT CAT AAA CTT AAG CCA AAT CAA ATT CCG TTA TTG AAA GAG AAC ATC CAT GAT TTA ATT
522 Phe Ala Leu Asn Phe Gly Asn Lys Asn Gln Leu Arg Val Phe Thr Leu Ser Lys Val Ile Leu Asp Ser Gly Ile Pro Gln Gln
4249 TTC GCA TTA AAT TTT GCG AAC AAA AAC CAA TTG CCG GTG TTT TTC ACT TTA TCT AAG GTG ATT TTG GAC TCC GGT ATA CCT CAA CAA
551 Val Gly Val Leu Pro Val Ile Gly Asp Asp Pro Met Asp Leu Leu Leu Ala Glu Lys Phe Tyr Trp Ile Ala Glu Lys Ser Ser Thr
4336 GTT GGA GTT TTG CCC GTT ATA GCA GAT GAC CCA ATG GAT CTG TTA CTC GCT GAG AAA TTT TAT TCG ATT GCT GAG AAA TCA AGC ACA
580 Gln Glu Ala Leu Ala Ile Leu Tyr Lys Tyr Phe Glu Ser Ser Asn Ser Pro Asp Glu Val Asp Asp Leu Leu Lys Val Glu Val Pro
4423 CAA GAG GCA TTA GCA ATA TTG TAT AAA TAT TTT GAA TCA AAC AGT CCA GAT GAA GTT GAT GAC TTA TTA GAT AAA GTG GAA GTA CCC
609 Glu Asp Tyr Lys Val Asp Tyr Asn His Val Leu Asn Lys Phe Ser Ile Ser Thr Ala Ser Val Ile Phe Asn Gly Val Ile Tyr Asp
4510 GAA GAT TAT AAA GTG GAT TAT AAT CAT GTG TTA AAC AAG TTT TCT ATA TCA ACT GCT TCG GTC ATT TTC AAT GGG GTT ATT TAC GAT
638 Leu Arg Ala Leu Asn Trp Gln Ile Ala Met Ser Lys Gln Ile Ser Gln Asp Ile Ser Leu Ile Lys Thr Phe Leu Arg Gln Gly Pro
4597 TTA AGA GCA CCA AAC TCG CAG ATT GCA ATG AGT AAA CAA ATA TCC CAG GAC ATT TCA CTT ATT AAA ACT TTC TTG AGA CAG GCA CCA
667 Ile Glu Gly Arg Leu Lys Asp Val Leu Tyr Ser Asn Ala Lys Ser Glu Arg Asn Leu Arg Ile Ile Pro Leu Glu Pro Ser Asp Ile
4684 ATA GAG GGT AGA TTG AAA GAT GTT CTT TAC TCT AAT GCA AAA TCA GAA CGC AAT TTA CGT ATA ATT CCA TTA GAA CCT AGT GAC ATT
696 Ile Tyr Lys Lys Ile Asp Lys Glu Leu Ile Asn Asn Ser Ile Ala Phe Lys Lys Leu Asp Lys Ala Gln Gly Val Ser Gly Thr Phe
4771 ATT TAC AAG AAA ATC GAC AAG GAA TTA ATA AAC AAT TCA ATT GCA TTC AAG AAG CTA GAT AAA GCG CAG GGT GTG TCT GCA ACA TTT
725 Trp Leu Val Ser Asp Phe Thr Lys Ser Ala Ile Ile Thr Gln Leu Ile Asp Leu Leu Leu Lys Lys Ala Ile Gln Ile

~~FIG. 1A~~ (cont.)

4858 TCG CTA GTG TCG GAT TTT ACC AAG TCA GCA ATA ATT ACT CAA TTG ATA GAT TTG TTA TTG CTT CTC AAA AAG AAA GCA ATT CAG ATA
 Arg Ile Ile Asn Thr Gly Asp Thr Asp Val Phe Gly Lys Leu Lys Thr Phe Lys Leu Thr Ala Leu Thr Asn Gly Gln Ile Asp 754
 4945 ACA ATT ATT AAT ACT GCG GAT ACA GAT GTT TTT GGA AAA TTG AAA ACA AAG TTT AAA TTA ACC GCC TTA ACA AAT GCA CAA ATT GAT
 Glu Ile Ile Glu Ile Leu Lys Lys Ser Asn Ala Ser Ser Ala Asn Asp Glu Leu Lys Lys Met Leu Glu Thr Lys Gln Leu Pro 783
 5032 GAA ATT ATT GAC ATT TTG AAA AAA TCC AAC GCT TCA AGT GCA AAT AAT GAT GAA TTG AAA AAA ATG CTT GAG ACT AAG CAA TTA CCT
 Ala His His Ser Phe Leu Leu Phe Asn Ser Arg Tyr Phe Arg Leu Asp Gly Asn Phe Gly Tyr Glu Glu Leu Asp Gln Ile Ile Glu 812
 5119 GCT CAT CAC TCT TTT TTG CTA TTC AAC TCT AGA TAT TTT AGA TTG GAT GGA AAT TTT GGA TAC GAG GAA TTG GAT CAA ATT ATA GAG
 Phe Glu Val Ser Gln Arg Leu Asn Leu Ile Pro Asp Ile Met Glu Ala Tyr Pro Asp Glu Phe Arg Ser Lys Lys Val Ser Asp Phe 841
 5206 TTT GAA GTA TCT CAA AGA TTG AAC TTA ATC CCG GAC ATC ATG GAG GCA TAT CCG GAT GAG TTT AGG TCG AAG AAG GTA AGT GAT TTT
 Asn Leu Val Leu Ser Gly Leu Asp Asn Met Asp Trp Phe Asp Leu Val Thr Ser Ile Val Thr Lys Ser Phe His Val Asp Glu Lys 870
 5293 AAT CTG GTT TTG TCT GCA TTA GAC AAT ATG GAC TCG TTT GAT TTG GTG ACT TCC ATA GTG ACA AAA TCA TTC CAT GTC GAC GAA AAA
 Arg Phe Ile Val Asp Val Asn Arg Phe Asp Phe Ser Ser Leu Asp Phe Ser Ile Asp Val Thr Thr Tyr Glu Glu Asn Ser 899
 5380 AAT TTT ATT GTT CAT GTT AAC AGG TTT GAT TTT AGC TCA TTG GAT TTT TCA AAC TCG ATT GAT GTA ACG ACT TAT GAA CAA AAT AGT
 Phe Val Asp Val Leu Ile Ile Leu Asn Pro Met Asp Glu Tyr Ser Gln Lys Leu Ile Ser Leu Val Asn Ser Ile Thr Asp Phe Leu 928
 5467 CCA GTT CAT GTA TTA ATA ATT TTG AAC CCT ATG GAT GAA TAT TCT CAA AAA TTG ATA AGC CTT GAT AAT AGC ATT ACA GAT TTT CTG
 Phe Leu Asn Ile Arg Ile Leu Leu Gln Pro Arg Val Asp Leu Lys Glu Ile Lys Ile His Lys Phe Tyr Arg Gly Val Tyr Pro 957
 5554 TTC TTG AAC ATT AGA ATC TTA CTA CAA CCA AGA CTG GAT CTG AAA GAA GAG ATC AAA ATT CAC AAG TTT TAT CCG GGT GTG TAT CCT
 Gln Pro Thr Pro Lys Phe Asp Ser Asn Gly Lys Trp Ile Gln His Tyr Ser Ala Gln Phe Glu Ser Ile Pro Ser Asn Val Thr Tyr 986
 5641 CAA CCG ACT CCC AAA TTT CAT TCC AAT GCG AAG TGG ATC CAA CAT TAT TCA GCT CAA TTT GAA AGT ATT CCA TCC AAT GTG ACC TAT

FEED - IA (cont.)

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Ser Thr Glu Leu Asp Val Pro His Lys Trp Ile Val Val Pro Gln Leu Ser Ser Met Asp Leu Asn Thr Ile Asn Phe Ser Glu Ser 1015
 5728 TCT ACT GAA TTA GAT GTT CCA CAT AAG TCG ATA GTT CCT CAA CTG AGT TCG ATG GAT TTA AAC ACA ATC AAT TTC AGC GAA AGC
 His Ser Val Asp Ala Lys Tyr Ser Leu Lys Asn Ile Leu Ile Glu Gly Tyr Ala Arg Asp Ile His Thr Gly Lys Ala Pro Asp Gly 1044
 5815 CAC TCT GTT GAT GCA AAA TAC TCT CTA AAA AAT ATA TTA ATT GAA GCA TAT GCT AGA GAT ATT CAT ACT GGG AAG GCC CCT GAT GGT
 Leu Ile Phe Arg Ala Phe Asn Lys Asn Tyr Ser Thr Asp Thr Leu Val Met Thr Ser Leu Asp Tyr Phe Gln Ile Lys Ala Tyr Pro 1073
 5902 TTA ATC TTT AGA GCT TTT AAT AAA AAT TAC TCA ACT GAT ACT TTG GTG ATG ACT TCC TTG GAC TAT TTT CAA ATC AAA GCG TAT CCT
 Ser Ile Phe Asn Phe Ser Thr Ser Asn Asp Thr Leu Leu Ser Ala Ser Glu Asn Lys Tyr Gln Ala Asn Thr Glu Leu Glu 1102
 5989 AAT ATT TTC AAC TTT ACT ACG ACC TCA AAT GAC ACA TTA TTG TCT GCA TCG GAA AAC AAA TAT CAG CTT AAT ACC GAG GAA TTG GAG
 Ser Ile Glu Val Pro Val Phe Lys Ile Asp Gly Ser Thr Ile Tyr Pro Arg Val Met Lys Ser Gly Asn Asn Lys Pro Met Leu Thr 1131
 6076 AIC AIT GAG GCG CCA GTT TTT AAA AAT GAT GCA TCG ACC ATA TAT CCA AGG GTA ATG AAA TCT GGC AAC AAT AAG CCA ATG CTG ACG
 Arg Lys His Ala Asp Ile Asn Ile Phe Thr Ile Ala Ser Gly Gln Leu Tyr Glu Lys Leu Thr Ser Ile Met Ile Ala Ser Val Arg 1160
 6163 AGA AAA CAT GCA GAT ATA AAT ATT TTT ACA ATT GCT AGT GGC CAA CTT TAT GAA AAG TTA ACT AGC ATT ATG ATT GCG TCA GTA ACA
 Lys His Asn Pro Ser Leu Thr Ile Lys Phe Thr Ile Leu Glu Asp Phe Val Thr Pro Gln Phe Lys His Leu Val Glu Leu Ile Ser 1189
 6250 AAA CAT AAC CCT AGC CTG ACA ATA AAA TTC TGG ATT TTG GAA GAT TTT GTG ACC CCA CAA TTC AAA CAC TTG GTA GAG CTT ATC TTA
 Ile Lys Tyr Asn Val Glu Tyr Glu Phe Ile Ser Tyr Lys Trp Pro Asn Phe Leu Arg Lys Lys Gln Lys Thr Lys Glu Arg Met Ile Trp 1218
 6337 ATA AAG TAT AAT CTC GAA TAT GAG TTT ATT AGT TAC AAA TCG CCC AAT TTC TTG AGA AAA CAG AAA ACC AAA GAA AGA ATG ATT TGG
 Gly Tyr Lys Ile Leu Phe Leu Asp Val Leu Phe Pro Gln Asp Leu Asn Lys Ile Ile Phe Ile Asp Ala Asp Gln Ile Cys Arg Ala 1247
 6424 GCG TAT AAG ATT TTG TTT TTG GAC GTT TTG TTC CCA CAA GAT CTC AAC AAG ATT ATA TTC ATT GAC GCC GAT CAA ATA TGT AGG GCA
 Asp Leu Thr Glu Leu Val Asn Met Asp Leu Glu Gly Ala Pro Tyr Gly Phe Thr Pro Met Cys Asp Ser Arg Glu Glu Met Glu Gly 1276

~~TABLE~~ - IA (cont.)

Fig - 1A (cont.)

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1 --MRAVAVLCVSVVLLALYIPUSGESSOSTITITIAHAKIOTPLYLEIREILADEQAQADWRSCTKLOTVLNEHATESQ-QINAALELVKXSHVSP
1 --NRKGFNFARATLITVOYRAK-----PUDVQIARIFKAPSFSAIAESLICEKKEGHNHLSOLDLADENTENELY-INVUNSLKREYVSDSE
1 --MSFARFTIYIYIAVAVLUNFVKATENN-----HFKLEVEASKEIDELPSPIEALVGFNDSTEQTETETIFGLCDTEVELEDDASQCEIYSTVINSLGTDQ
1 --NRDLALVLLLCAPIRAMT-----YSTRYGIPESAQWNSILVHLIGDVHQLLNLIPVUGLDDDEIDIOENLYALTSNVLRRERTOKEDVAD

98 QMPLARLVVSMHSLTPRIQIFEQLAEEELRSSG-----SSQSFTHAQVGSALA-----CSFHELOKLEVPLEKDSLDAPVVTYSFDKIFPGSENNR
99 --BASSQCSSTQUSGAPXIQAFSSIVQSR-----TQODDTNLDDEESQ-----VCFSDMPDPLFSQTSKNP---LDTEVVKTS---AIGI
97 --DADTIFHDMINXKHTPRIAHYDNISDVLTKEGDRUKSEGANDSECAVETKEGOIQTNLTYNDKINCSANDLEFARADLSSHSTILFDRIGKS-KDAP
98 --LDELTYASUTPUGHLOHDISSNAEQDDAN-----SSYFVLCGRREKPD-----DVFNLSKNDLTIOOKVDPDVIOPIDVVIGTN-SEAP

185 --VWLYGDLGSSQ--FRANKKLEKERNACRIRIIRHQLAKXDMR--PVRLSGYGVELHUKSTETKSODDAPKPEAGSTSDLANESDVQGFDFKVLKQ
167 --PIAVVVFSTED--LIRHELYKLALEGCKHIVIRYSPSSSKLHAKVWGFCTHVSIAKRTDYLVDPREFPRECONPASFTSS-----R--
196 --LVILYGSPEEL--TKPLILYPOHAKGUKLVWRYIPLGIXKD--SISGYGUSLKKKEKIDYSGAEGN--P--
167 --ILILYGCPTVIDSOFEPENANTENEMNAGEGCFRTWRSTCSLDG--NSVENELHPLEITLQNGSRHSSIPQIUK-----

281 --KHPTLIRALDQPRQRLLOGHDETAQAKAMEFQDLGQAAANAAETQGD-----ETHQILOYYTAHNFPHIARTLALHKVIDGLRNVKHNTEAFGRSLHVA
253 --NRSNERLFGHTSDSLQVTPDXIALPDLAATQSISSAOWLS-----AFRELTQDFPIYAHYLSIQPDUSHHLISELN---QFOSQIUP
263 --NYGASRDETEINDSOELVLVNEKSTELGVKLISFILSNRYKS-----TKIDLDTLTITNPKFIPYIARLPKLTINTEKVKSKVLG--NEDIGLS
241 --LLTTPKXELVGAHNDQCHQDEPEPEIRELDRVTSLSISEFVQIXKDITATAMFTKSIVHNFPLTSKQCIKVSUNXKDIITSNE---ELNFKGFD

376 --PDGALFINGLFFDADTMDLYSLETURSHRVLESKSNVVRGSLASSLALDLTASSKKEFAIDIR-----DIAVQMVN
335 --EGHNITINGLSLDLEEDAFSILSLIKKEDHDFRFEALGKSSKVLNIVYHVFANEDSDFKXVBFHCQDDIED-----HKNLHNVN
351 --QDSYGIYINGSPIPLELDIYMGTRIMEELQTKWMDVVLGFDIVQAKHLIAKPAULSAVXQTQERNGRTLNGNENRFRKVEHEFKKGSSEKCGVLFFN
333 --YNALGLYINGQNWKTTSITPYNALTAKTEVQSLUKLTNULOELFKHQCHDSKPLHNFQFSLGRLQNLQPIKNDLHTIPG-----FSSESITFN

11

DMUGGT 846 TELHURVVISORVLGNNKNSORLVLENGRIIGPSSDESFDSDFAJLARTSSTGSDKVRQVLKESQDVN-----EEFNSDTLLKLYASLUPRO
SPUGGT 765 AUFANKSAVWKEIGVTECKXSALLINGRMIGCSFSDS-LHITADLKQKQKEIDHETLSKLSRIAGSSRRKXNSRATSFUSSYLLKLESTPMSTSSPINE
CACKRE5 773 ENCHMETKQPAHHSFIFMNSRIFRLDGHFGEEDQIIEFVSORLMLTPDIHEAFDEFRS KKVSDFNVLVSG-LDNMDWFCIVTISIVTKSFHVDENR
SCCKRE5 753 LKHWLPDIPAFHELOKGSFIALNGRFILLKMKMGCKQKHSKAKIKKEAHRJDSVADLIFPGFSQEIINPDILIEHSSILTRFIQGTHTYNNGIDYT

FREE - 18 (cont.)

DmUGGT	1325	LF	LD	VL	FL	PL	VR	VI	FV	DA	IV	DI	KL	DN	LC	GP	VT	FF	CD	SR	NE	GFR	FK	CG	VS	NG	---	RR	YS	AL	YV	DL	RR	FK	IA	GD	LR	LG
SpUGGT	1242	LF	LD	VL	FL	PL	VR	VI	FV	DA	IV	DI	KL	DN	LC	GP	VT	FF	CD	SR	NE	GFR	FK	CG	VS	NG	---	RR	YS	AL	YV	DL	RR	FK	IA	GD	LR	LG
CaKRE5	1223	LF	LD	VL	FL	PL	VR	VI	FV	DA	IV	DI	KL	DN	LC	GP	VT	FF	CD	SR	NE	GFR	FK	CG	VS	NG	---	RR	YS	AL	YV	DL	RR	FK	IA	GD	LR	LG
ScKRE5	1186	LF	LD	VL	FL	PL	VR	VI	FV	DA	IV	DI	KL	DN	LC	GP	VT	FF	CD	SR	NE	GFR	FK	CG	VS	NG	---	RR	YS	AL	YV	DL	RR	FK	IA	GD	LR	LG

SUBSTITUTE SHEET (RULE 26)

11/24

DMUGGT 1422 YQALS QDPNLSNL DQDLPNM IN QVAINSLPDDHLWCCTNCS DSIFKTAHVIDLCNHPCKEAKITARORIVPEHNDYDDELKTLMSRIEDHENSUSRD
 SPUGGT 1338 YQLLSADPNLSNL DQDLPNM IONLIPISLPDHLWCETNCS DESIKTAKTIDLCNPLCKEKNDDPARROVSEHTSYDNEIASVLOTAS SQSDMEFEZ
 CAXRES 1321 YQKLS SDPNLSNL DQDLPNM QRLNIPISLPDHLWCETNCS DXSLEDAKTIDLCNPLPEHNDARARLLPEWFEYECEIEPLVSLVQNH TAMBVVQ
 SCXRES 1279 YQRTIS QDANSLVNH QDILVNNIQLAVPIR-----FLKG--S-----YXKLVINDECVSEHKKKINKF ASSPGDECVPGESVSK

DMUGGT 1522 SAVD DSVDDS VEV T VTPSH EPRH GEZ
 SPUGGT 1438 KDNN SSPDEL-----
 CAXRES 1421 EIEHIDGCEQEFQK QESND DDFIHDEZ
 SCXRES 1352 YQDS DNAAFDHDEL-----

7 1 8 7 0 5 (cont.)

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7123 AC 7A

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319 Gln Phe Ile Arg Glu Glu Arg Glu Glu Ala Tyr Leu Gln Lys Met Ile Ala Lys Asn Ile Leu Arg Ile Asp Glu Phe Gln Asn
1208 GAA TTT ATT ACA GAA GAA AGA GAA GCT TAT TTA CAA AAA CAA ATG ATT GCT AAA AAT ATT CTG CGT ATT GAT GAA TTT CAA AAT
348 Leu Ser Lys Asn Asn Thr Thr Ser Gly Ala Ser Arg His Pro Tyr His His Ser Asn Asn Lys Lys Asn Asn Gly Gly Asp
1295 CTT TCC AAA AAT AAT ACT ACT GGT GCA TCT CGT CAT CCA TAT CAT CAT CAC AGT AAT AAT AAT AAT AAT AAT AAT GGT GGT GAT
377 Gly Gly Ser Ser Met Ala Ala Leu Lys Tyr Thr Pro Lys Asn Ile Leu Lys Lys Thr Leu Ser Arg Phe Glu Phe Thr His Glu
1382 GGT GGT GGT TCT AGT ATG GCA GCA TTA AAA TAT ACT CCA AAA AAT AAT TTA AAG AAA ACA TTA TCA AGA TTT GAA TTT ACT CAT GAA
406 Asn Ser Ser Ser Glu Glu Ile Tyr Glu Leu Lys Thr Lys Gln Pro Tyr Tyr Asp Asp Gln Leu Ser Leu Thr Ser
1469 AAT TCT TTA TTA TCA GAA GAA AAT TAT GAA TTG AAG ACT AAA CAA CCA CCT TAC AAA TAT GAT GAT CAA TTA TCA TTA ACT TCA
435 Ser Thr Ser Thr Ser Gly Ser Gly Ser Gly Gln Val Lys Phe Gly Gly Ala Arg Ile Ser Asp Gly Ile Asn Gly Gly Ser Leu
1556 TCT ACA TCT TCT ACT TCT GCA TCT GCA TCT GCG CAG GTG AAA TTT GGT GGA GCA AGA ATT TCT GAT GCG ATT AAT GGA GGT TCA TTA
464 Pro Asp Arg Phe Ser Leu Phe His Ser Glu Ser Glu Thr Ile His Ala Pro Asp Ile Pro Ser Leu Val Ser Pro Gly Gln Ser
1643 CTT GAT AAA TTT TCA CTT TTC CAT TCT GAA TCA GAA GAA ACT ATT CAT GCC CCC GAT ATT CCA TCA TTA GTA TCA CCA GGT CAA TCT
493 Val Arg Asp Leu Phe Arg Asn Gly Glu Glu Thr Trp Trp Leu Asp Cys Thr Cys Pro Thr Asp Ser Glu Met Lys Met Leu Ala Lys
1730 GTT CGA GAT TTA TTT AGA AAT GGT GAA GAA ACT TGG TGG TTA GAT TGT ACT TGT CCT ACT GAT TGG GAA ATG AAA ATG TTG GCG AAA
522 Ala Phe Gly Ile His Pro Leu Thr Ala Glu Asp Ile Arg Met Gln Glu Thr Arg Glu Lys Val Glu Leu Phe Lys Ser Tyr Phe
1817 CTA TTT GAT ATT CTT TTA ACT GGT GAA GAT ATT CGA ATG CAA GAA ACT CGT GAA AAA GTT GAA TTA TTT AAA AGT TAT TAT TTT
551 Val Cys Phe His Thr Phe Glu Ala Asp Lys Glu Ser Glu Asp Tyr Leu Glu Pro Ile Asn Val Tyr Ile Val Phe His Asp Gly
1901 GTT TGT TTT CAT ACT TTT GAA GGT GAT AAA GAA TCT GAA GAT TAT TTA GAA CCG ATA AAT GTT TAT ATT GTT TTC CAT GAT GAT GAT
580 Ile Leu Thr Phe His Phe Ser Pro Ile Ser His Pro Ala Asn Val Arg Arg Val Arg Gln Leu Arg Asp Tyr Val Asp Val Ser
1991 ATA TTA ACG TTC CAT TTT TCA CCA ATT TCT CAT CCA GCA AAT GTT AGA AGA GAT TAT GTC GAT GAT GAT GAT
609 Ala Asp Thr Leu Cys Tyr Ala Leu Ile Asp Glu Ile Thr Asp Gly Phe Ala Pro Val Ile His Gly Ile Glu Tyr Glu Ala Asp Ala
2078 GGT GAT TGG TTA TGT TAT GCC TTA ATC GAT GAA ATT ACC GAT GGT TTT GCC CCC GTG ATT CAT GCA ATT GAA TAT GAA GCT GAT GCT
638 Ile Glu Asp Ala Val Phe Thr Ala Arg Asp Thr Asp Phe Ser Ser Met Leu Gln Arg Ile Gly Glu Ser Arg Arg Lys Val Met Thr
2165 AAT GAA CAT GCG GTT TTC ACT GCT ACA GAT AAT GAT TTT ACT AGT ATG TTA CAA AGA ATT GGT GAA TCA AGA ACA GAT ATG ACT
667 Leu Met Arg Leu Leu Ser Gly Lys Ala Asp Val Ile Lys Met Phe Ala Lys Arg Cys Gln Glu Ala Asn Ser Ser Ser Gly Tyr

FIG. 2A (cont.)

SUBSTITUTE SHEET (RULE 26)

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1 HSSSSSSSSSPALSRNSLSTANVTSMKTEDHTGLIDHROHPC
1 HSSLSSTSPDSSDLPRSKSVNTAISMKWCXPKLENIRQISDA
1 -KSDSESITQHSITNPIPRSDVDDHHRHOTHDCAISDSSE
SCALR 1
SCALR 2
CaALR 1

100 GODETVANHOLRASAITSNARPSRLAMSHHQRLVESH
99 AEAELVXRYQLRSFALISSNARPSRLAKSEHOKQURVESIAPIELKN
92 -KDRITPHSLSGDDTINSCHKXRNHNSSRKDPYUKNDIDN
SCALR 1
SCALR 2
CaALR 1

196 ESKSDTHSLANPKKRTYSTISHSSINPAVLLTKSPKSDA
195 ESEHGHFNCAKPKRRTYSTISTHSSVNPILLERYSOKSDWGP
191 DLVSPHAKKINDSEDIINTSITANMKXGIGATIDVGIGI
SCALR 1
SCALR 2
CaALR 1

295 EEVAQFAN---AENSOPLASTQV PNEQK
294 EEVAQISH---AERNISLANHQRHSER
290 DEFIREEREATLOKQOMIAKULRIDEFQNLKNNHTISGASHPINHE
SCALR 1
SCALR 2
CaALR 1

368 EDEHEKIPSLHGGISCKNNKEGEENENIPSHDPAYCSIGCTDQ
367 ESVREDDKPDLLHDVTFGRNNKEGEKENDSSISRATITQTEIO
390 TKQQPPIMDDQLSLSSSSISGSGSQVXFGG-ARISDGINGG
SCALR 1
SCALR 2
CaALR 1

468 RCIAKAFGINHPLTAEDIRHOETREKVELFKSYFVCFHCFENDKES
467 RCIAKFGINHPLTAEDIRHOETREKVELFKSYFVCFHCFENDK
489 RCIAKAFGINHPLTAEDIRHOETREKVELFKSYFVCFHCFEND
SCALR 1
SCALR 2
CaALR 1

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ScALR 1 568 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 ScALR 2 567 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 CaALR 1 589 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----

ScALR 1 662 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 ScALR 2 661 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 CaALR 1 689 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----

ScALR 1 714 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 ScALR 2 713 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 CaALR 1 789 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----

ScALR 1 813 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 ScALR 2 812 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----
 CaALR 1 885 IDDI TD SFAPV IQS IEYEADATED SVFMARDNDF AANLORIGE SRRKTNLNR LLSGKADV KHF AKRCODEANGIGPALTSO IN DANLQARD-----

----- 2B (cont.)

1 TTATATAACATGATTNGAATAACAATGGTATANTTGAATGCCAAGCAATAT

52 TGAATTGTATGGATTGGTAACAATAAGATCATATTGGTGTGGTCAGGGGAATGGGACAAGATAAAATTTGAAGTCACTGCTGAACTTCAAAAACAAGTTGTTGAGAAATATTTTCC

167 AATTGATACCCCATGGCAACCCACAGAGGAATTTCTCAAGCTGAATGGTTGAAATTTTATGAAATGGTGGCAGATTACTCATTTGGCATATGGGCAGGTCACCATTTAGGATT

282 TGAGCAAGAATATGAGACATCATTTGGAGAAATACCATGCTAATGATGCTCTGTCAAATAAACAATAAGAAGATATCGAACATGAGTTGTTACATCATCAACAAGAG

397 ATTGAAGAGACTCAGCATAGATCGAGTCGATTGMAAAATTTGCTGGTGATTACTGGTCAGAGATCAATATCGACAATCTTAAACCAAAATATAGAAAAACAACAGAAATAGTAGAG

512 AGGTTAGTAAGAGAAACCTTNAAAACAACACAGGAGCAACNCTTAGCTGGCTATATAGAAGTAGAAATAGAAATCANGATCAATATAAAAGACGCCACCAACAGCGCTACTACT

627 ACTACTACATTTTGAACAACATTTGCTGGGAAGTTGAATGATTGACATGTGAGCCACATAGCTTAGGTATAGTTGCTTGAACCTAAACACCGAAGTTCTTGTATTAAAGATAG

742 AATTCCTCTCTCTCAAAAAGCTGCAAAATTGACACACACAGTAGAAGTATTTTGACGGGTATATTGGCAAGTCAAAATTGAATGTGTGTCATTTCAATCTCTACAAAAGATACAC

857 AAAATGAATAACGAATTAATAATAAGTTGTCATCATCGTCAAAATAATGACAGAAAAATACATTTATCCTATGGAATTGTAATGTGATTATGATATGCTTGTAAATTGAGGTCGTA

972 GTAGTAGTAGTGTGTTTCATTTATGCAACATTAACCAACATAACAGACATAAGAGGGGGGGAGGAATTGATTGCTCTACTAGTTTCTTCTATTACAAGAATTTCTTTTG

1087 TTTTACAGTAATTTAAATGTAATAATGTAATGTAATAATGTTTGAATGATTTTCAATTAATTTTCGTTACAAAACAAGAAGATGAAAAAATTTTCATTATGGA

1202 ATTTTGGGGATATTGAATCGTGTGTTAAATACTTTGTCTATTCAATTCAGCTTGAGTTTACTAGTTTGCACCTGGTTGCCACTAGTTTGGCCACCAAGAAGTTG

1317 GACTAAAGTTTATATCTCTTATATATAATTACCTTAATAGTCACTTCCTTCTTCATTCTTGTAGTCTTTGTTACATTTTGTGTTCTGTTCTGTTACTACTAACAC

1432 AACACAATATTTTTTTTAAATCCCTCCTCACTCAATCAACACACACACCCCTATTTCTTTCTCTTCTACTCTTGGTGTAACCTTTTGGCTGGCCTCTTTCTTTTG

1547 CTATTTTCAAATTTCTTAGCTCATTTTAAATTTATTTCAATTTGTTTCCATTTATTTCCATCTTTGCTTTTCCATTTATTTATTTTCTTTTCTTTTAGTTAGCT

1662 CTAAATTCNACTTCTTACTTCTAATCTGAAATCTAACAACTAAAAAAGACAGAGTGAATAAGGTGAGAAATTTGCTRAAAAAAATAGACAGACAGAAAAAAGTA

1777 ACGMACCAANGACAGGAGAAAAAATTCACACACAGGACAAACATCAACAAACATTACATCAGCAACAGACAGACCAATATACATTAAACCAATCACACTGAAAC

1892 TTACTCATAACTACTGCTCATATCTTCTCTTTTTTTTTTGTGTCATATTGAAGAAATAGAAACCAATAGAACCACTCATTTATATCTTAATATCAACAATCCAAAC

Met Glu His Pro Ala Ala Leu Arg Thr Phe Ser Thr Gln Ser Thr Ser Ser Leu Asn Ser Val Ser Thr Val Ser Ser Ser Arg

2007 ATG GAA CAT CCA CCA GCA GCT CTC AGA ACA TTT TCA ACC CAA TCA ACT TCA TCT TTG AAT TCA GTA ACT ACT GGT TCG TCT TCA AGA

Ile Val Ser Leu Gly Pro Val Asn Ile Asn Asn Phe Asn Lys Pro Ser Thr Pro Lys Asp His Leu Phe Tyr Arg Cys Glu Ser Leu

2094 ATT GTT TCT CTG GGC CCA GTC AAT ATA AAC AAT TTC AAT AAA CCA AGT ACT CCC AAA GAC CAT TTA TTC TAT CGA TGT GAA TCA CTA

Lys Arg Lys Leu Lys Ile Pro Gly Met Glu Pro Phe Leu Asn Gln Ala Phe Asn Gln Ala Glu Gln Leu Ser Glu Gln Ala

2181 AAG CGA AAA CTA CAA AAA ATC CCT GGC ATG GAA CCA TTT TTG AAC CAA GCT TTC AAT CAG GCT GAA CAA CTC AGT GAA CAA CCA GCA

Leu Ala Leu Ala Gln Glu Arg Ser Asn Gly His Ser Asn Gly Lys Arg His Gln Ser Leu Asp Gly Ala Met Asn Arg Leu

2268 TTG GCT TTG GCA CAG GAA AGC AAT GGA CAT AGT AAT GGC AAA CGT CAT CAA TCA TTA TTA GAC GGT GCC ATG AAT AGA CTT

Ser Val Gly Ser Asp Ser Ser Ile Gln Gly Ser Leu Thr Arg Met Ala Thr Asn Ala Ser Thr Ser Ser Leu Ile Ser Gly Met

2355 TCA GTT GGT TCT GAT AGT AGT TCG ATT CAA ATG GCT ACC AAT GCG TCA ACG TCA TCT TTA ATC AGT GGT ATG

7107 7A

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File - 3A (cont.)

Ser Ser Thr Thr Asn Leu Leu Glu Ser Ile Asn Asn Ser Arg. Lys Asp Asn Thr Leu Pro Leu Glu Leu Lys Gly Arg Val Tyr
 3660 ACT TCA TCG ACT ACT AAT TTG TTG GAA TCA ATA AAC AAT TCC CGA AAG GAT AAC ACA TTG CCA TTG GAA TTA AAA GGA AGA GTT TAT
 Ile Ser Glu Ile Tyr Asn Ile Ser Ala Pro Asn Thr Thr Pro Gly Ser Thr Leu Ile Ile Ser Trp Ser Gly Arg Lys Glu Ser Gly Ser
 3747 ATA TCG GAG ATT TAT AAC ATT TCC GCT CCA AAC ACT CCT GGC TCA ACC CTA ATC TCA TGG TCA GGT AGA NAG GAA AGC GGC TCA
 Phe Thr Leu Arg Tyr Arg Ser Glu Glu Ala Arg Asn Gln Trp Glu Lys Cys Leu Arg Asp Leu Lys Thr Asn Glu Met Asn Lys Gln
 3834 TTC ACT TTG AGA TAT CGT AGT GAA GAA GGC AGA AAC CAA TGG GAA AAG TGT TTA CGT GAT TTG AAG ACT AAT GAA ATG AAT AMA CAA
 Ile His Lys Lys Leu Arg Asp Ser Phe Asn Thr Asp Ser Ala Ile Tyr Asp Tyr Thr Gly Ile Ser Thr Ser Pro
 3921 ATT CAT AAG AAG TTA CGT GAT TCC GAC CTG TCA TTT AAT ACT GAT GAC TCT GCC ATA TAT GAT TAC ACG GGT ATT AGT ACG TCA CCA
 Val Asn Gln Ser Thr Gln Gln Tyr Tyr Asp His Arg Gly Ser His Ser Ser Arg His Ser Ser Ser Thr Leu Ser Met
 4008 GTC AAT CAA TCA ACT CAA CAA CAA TAC TAT GAT CAT CGG GGC TCT CAC AGT TCC CGC CAT CAC TCA TCG TCA TCC ACT TTG AGT ATG
 Met Lys Asn Asn Arg Val Lys Ser Gly Asp Leu Ser Arg Ile Ser Ser Thr Thr Leu Asp Ser Phe Ser Asn Asn Leu Asn
 4095 ATG AAG AAT AAT AGA GTT AMA TCT GGT GAT TTG AGT AGA ATA TCT TCA ACT TCA ACA TTA GAT TCT TTC AGT AAC AAC TTG AAT
 Gly Ser Pro Asn Thr Thr Asn Pro Ser Leu Thr Ser Ser Asp Ala Thr Lys Thr Ile Pro Thr Phe Asp Val Ala Ile Lys Leu Leu
 4182 GGG TCA CCA AAT ACC ACT ANT CCA TCT TTG ACG TCT TCA GAT GCC ACC AAA ACA ATT CCA ACA TTT GAC GTT GCA ATT AAA TTG CTT
 Tyr Lys Ser Thr Glu Leu Ser Glu Pro Leu Ile Val Asn Ala Gln Ile Glu Tyr Asn Asp Leu Leu Lys Ile Ile Ser Gln Ile
 4269 TAC AAA TCG ACA GAA TTG TCA GAG CCA TTG ATT GTC AAT GCA CAA ATT GAG TAT AAT GAC CTT TTA CAG AAA ATT ATC TCC CAG ATT
 Ile Thr Ser Asn Leu Val Ala Asp Val Asn Ile Ser Arg Leu Arg Tyr Lys Asp Asp Glu Gly Asp Phe Val Asn Leu Asn Ser
 4356 ATC ACT TCG AAC TTG GTG GCT GAT GAT GTC ANT ATT ACT CGA TTG AGA TAT AAA GAC GAC GAA GGA GAC TTT GTG AAT TTG AAT TCA
 Asp Asp Asp Trp Gly Leu Val Leu Asp Met Leu Thr Ser Glu Asp Phe Tyr Gln Thr Ser Ser Asn Glu Lys Arg Leu Val Thr Val
 4443 GAT GAT GAT TGG GGG TTA GTG CTT GAT ATG TTA ACC AGT GAA GAC TTT TAC CAA ACA TCA AGC AAT GAA AAA CGA CTG GTG ACA GTG
 Trp Val Ser Stop
 4530 TGG GTT TCT TGA TTTAACTACAGGAACAAACGCTACCTTTGTTGGTGTGTGTATGTATGGGTGCTTTTTTTTTTTTCTGATGGTGTGACTTTGGACAGATA
 4641 AACAATTAAGAGTTAATGTTTGTGTGCGAAAATAAGCTGTTATAGATGGGTTCAATTAATCAATTTTCATATAGATATAAATGACACTTTGACGAAATATACTATTATATAA
 4756 TTTCCCTTTTCTTTGTTGTTAAGATTAAATGTTGGTCTTGTGATGTGTCGGTACACCAACCAATTAATAATCTAGTAAGACGGTAAATGGGTAGATGAGAAAAGGTCA
 4871 ATAGAGTTTATCTAATGTGGTGCATAATTAAGGCAACAGATAAATTTGGTAAACATTTTCTAAACGTTATTTGCCGCTTCCAGAGTCAAAAAAGAAATAAAGCTATATATTA
 4986 GTGCTAATAATAGTAGTAATACAAAACAGGTTTCAAGTTTTCCGCTCAAAACATCAAGCCATTGCTTATATAGATGACTATTCAATTAACAGGCAAAAAAAGCCATCATTT
 5101 GAAAAGACTCTCATATCAAGAGGTACTTCTAATACTAATCACTGTTGTTTTGATTATTAATGATTTGATTTCTATTGGTTGAACCTAACCCCAANTGGGTTTKTTGTTGGC
 5216 GGGTTGARAATGAATGCCATANATNATCAATTTGAAAAAANAANAANAANCTAATACACACACCCCAACCCCTTTCGNTTTATCA

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CaCDC 24 1 MEHPPANRITSTQSTSSLSUSVS TVSSSRIVSLGPVNIHMFHKSSEPPH
 ScCDC 24 1 -----HAIQTRFASGISDSD LKPKPSATSIIPHQVVMKKVETI
 SpCDC 24 1 -----HMERLQSPSQVIYNDENTVS-----

CaCDC 24 101 SNGKRNQSLDGMHNRISVGDSSISIQSLTRKA TNASTSSLSI SGPNSHSLF
 ScCDC 24 93 SNGARNRDSDDLAPILRSSSISIAKSLMSHEGISYTHSHPSATPHED
 SpCDC 24 49 -----ENRPS-----

CaCDC 24 201 DLR-----ICKKSVYDFLIAMVQLNFDDEKHEFTI SNVFSNHAQDILKIIDVH
 ScCDC 24 191 DLK-----VCKKSHVDFILCKKHFNENDELEFTISDVFAFSSQVHVE
 SpCDC 24 102 SLEHTHVCAISLYRFRHCKNELGLTDALFISI SEIKKPSA PAIRPOTHE
 -----HDVQUTDERSKUTREIT

CaCDC 24 287 ETERKYVQDLELCKYRQDMTEAENLSSEQLHLFPNLNELIDECERF
 ScCDC 24 288 ATERKYVQDLEILCKYRQCLDSHLITSEETMLFPNLGIDECERF
 SpCDC 24 200 ETELKYVQDLEILSHVHVDQOKQILSQDILSLHFTNLNELIDECERF

CaCDC 24 387 LKKSS-----LIDP CPELOSTILKPIORLCKYPLLLKELIM
 ScCDC 24 387 ARVDESORFIHNNKLELOSPFKPVORLCKYPLLLKELLAS
 SpCDC 24 299 LDKVAN-----LLEP SHEPPIPIPIORLCKYPLLLKELLGIE

CaCDC 24 484 GFNDACGELLFHGOVGVKDMEN-----EKENVAYLFKEMVFF
 ScCDC 24 476 GYRDSKFGELLIFDKVHJSTINS SSEPENREFFVLFKELIL
 SpCDC 24 386 GYSLQIFGCLLHVDVNVCKADI-----ERENVYLFKELILCC

-----STSSNLS
 -----JSSNITDNKSGSPH
 -----VVPNHMGSIATQIFRAGD

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CaCDC 24 553 -----SSYMLPSIHNSKDAALP-----DELKGRVLSSETHISAPNTEGS-----
 ScCDC 24 557 -----SYKXHSNSSSNWHLSSSSAAAIHSSSKSDHSSSSSSSLFSLSAHEPKDARGHIMKMLQIIPQNR-----
 SpCDC 24 482 PCHESFILKLARNEESHKELHNSVLNRLWKKEHGSPKDHSAASHPHVPVIRSSSQISKGYHSSDIYDLETHSDENVNSPTISISFSSKSSPPFIATSK

CaCDC 24 597 LIUSMSGRKESGFTLHYRSEELRNQHEKCIARDPKYEDKQLEKMLSDSLSFHDDSAIIDTIGISTSPVNOSSQOQYIDHRGSHSSSHSSSSSLSH
 ScCDC 24 633 LNIWESIKKEOGNFIKFKNEETDMHSSCLQQLINDUKNEQFMADHSS-----TSTSSAKSSSSXSPQIMHTPHHNSRQTHDSHASTSSSH
 SpCDC 24 582 DTKSATTDERPSPDFURLNSEESVGTSSLRTISQITSTLYSHDSSSTASIPSQISRISQVHSLNDINYNHROSHIRVYSGTDGSSVSIPTDITSSSTKQK

CaCDC 24 697 WKHHRVKSGDLSRISSTILDSTSNLNGSPHTHPSLESSDARKPPFDVAIKLJKSTELSEPLIUNAQIEYHDLQKISQIITSN--LVADDVN
 ScCDC 24 725 WK-----RVSDVLPKRRTHSSSEIKSISEYFKSIPESSLRHLSYHNSHNSWTSSEIFTDIEKVNHTDDIMHNSKISHI--HNHTSP
 SpCDC 24 682 QPDQPTINDCDVHRPROTSISAGHXSGSLPSKHTSLSSSSSTGSSVHHTVVKRLRLHEVSLVLVAKDITFEDDLAKVHKKIKLGGIPKQWPP

CaCDC 24 795 ISRLRIKDDGDFVNLNSDDHGVLDHMLSDFIQTSSEKRLVITVUS---
 ScCDC 24 813 LKIKVQDEGDFVVLGSDENHVAKEMPAENKFDHRLI-----
 SpCDC 24 782 RVRKXVDEGDFLQITSDQVLAFAFCTQFELHDPMHNGCHDVLHVVVF

--- 3B (cont.)

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PCT/CA00/00533

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CaKRE5
1 2 3 4
hisG
1 2 3 4
CaURA3
1 2 3 4

9.0 kb-
5.0 kb-
5.0 kb-

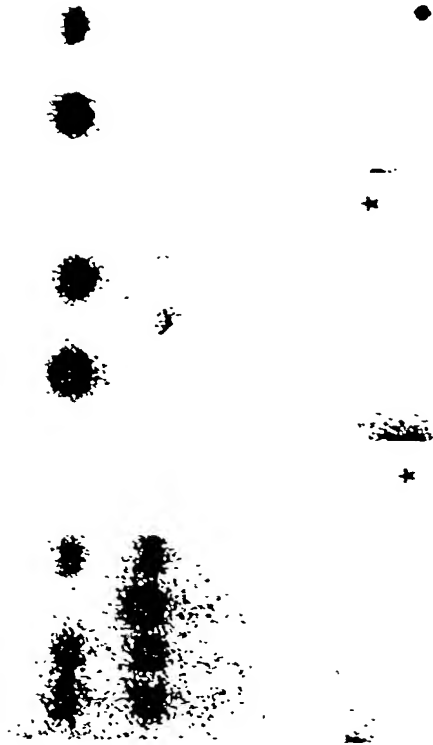


Fig. 4B

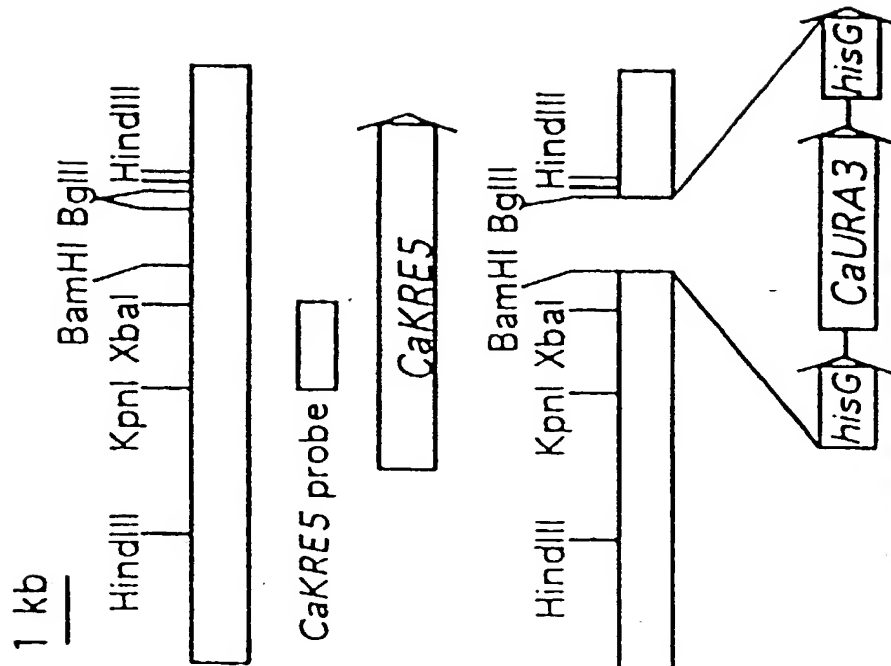


Fig. 4A

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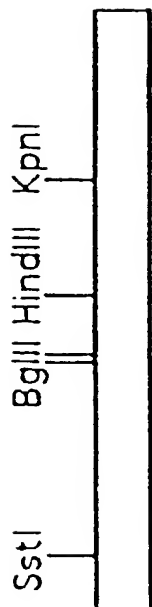
PCT/CA00/00533

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CaALR1 hisG CaURA3
1 2 3 4 1 2 3 4 1 2 3 4



FIG. 4D



CaALR1 probe

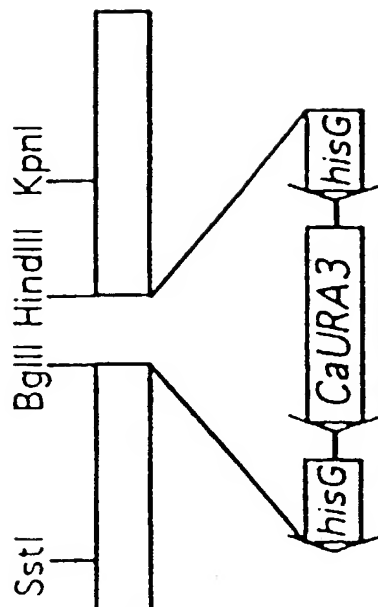
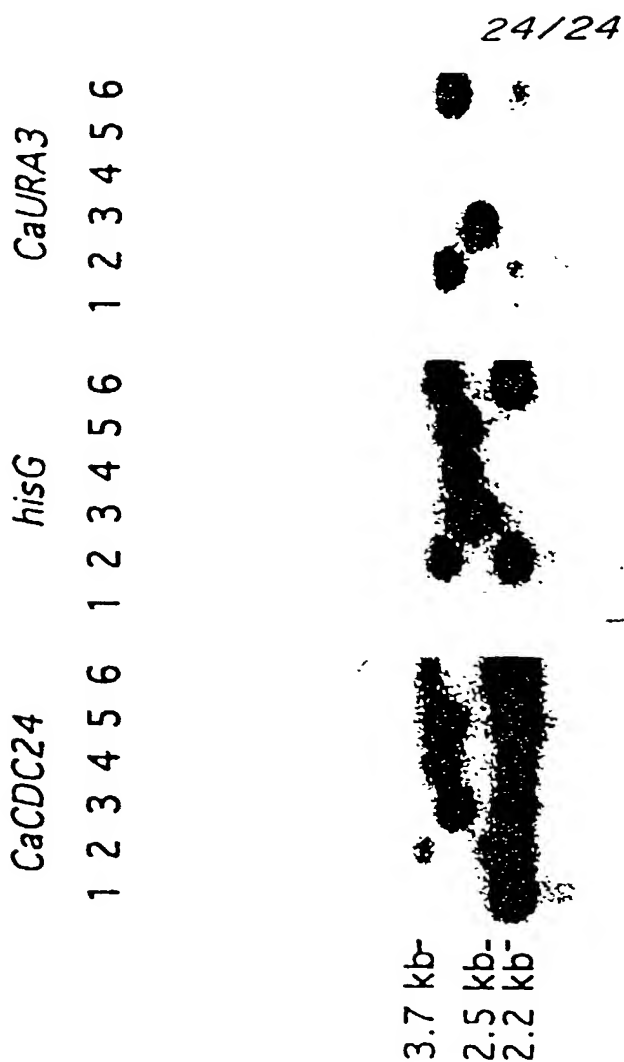



FIG. 4C

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CaCDC24 probe 

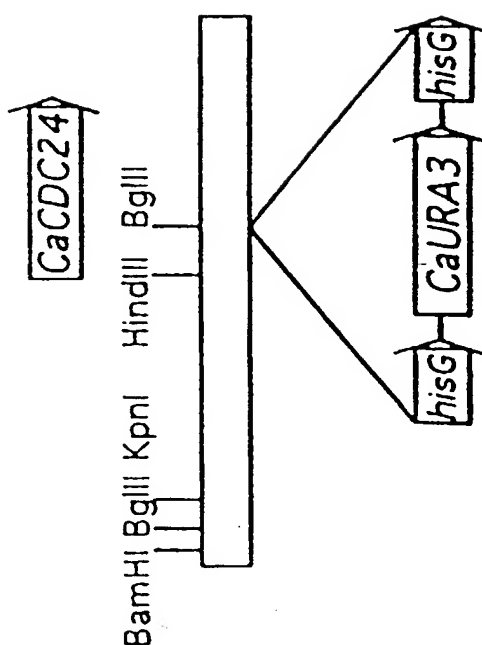


Fig. 4E

Fig. 4F